

GenCore version 5.1.3  
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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: December 4, 2002, 03:34:15 : Search time 57 Seconds  
(without alignments)  
2835.415 Million cell updates/sec

Title: US-09-784-340-2  
Perfect score: 2802  
Sequence: 1 MRSDKSLVFLQLQFCVGC.....KCFLESCQKFKRKIEKRE 527

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model DEV-xmlh  
-O=/cgn2\_1/USPFO.spool/US09784340/runat\_02122002\_122447\_18980/app\_query.fasta\_1.711  
-DB=Issued\_Patents\_NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blcsum62 -TRANS=human40.cdl  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MALEN=200000000  
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-NO\_XLPHY -NO\_MMAP -LARGEDUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THRADE=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/plodata/1/ina/5A.COMB.seq:\*  
3: /cgn2\_6/plodata/1/ina/5B.COMB.seq:\*  
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5: /cgn2\_6/plodata/1/ina/6B.COMB.seq:\*  
6: /cgn2\_6/plodata/1/ina/PCtus.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	61.8	2107	4	US-09-180-852-1
2	1399	49.9	1413	4	US-09-813-918-1
3	1131	40.4	2336	5	PCT-US92-00282-1
4	1068.5	38.1	2339	5	PCT-US92-00282-2
5	391	14.0	391	4	US-09-370-838-21
6	377.5	13.5	1190	5	PCT-US92-00282-21
7	318.5	11.4	1448	5	PCT-US92-00282-16
8	317.5	11.3	1008	5	PCT-US92-00282-10
9	297	10.6	1066	5	PCT-US92-00282-14
10	287	10.2	783	5	PCT-US92-00282-22
11	281.5	10.0	1561	5	PCT-US92-00282-25
12	274.5	9.8	2025	4	US-08-942-012B-23

13	272.5	9.7	1219	5	PCT-US92-00282-8	Sequence 8, Appli
14	271.5	9.7	1197	5	PCT-US92-00282-12	Sequence 12, Appl
15	265	9.5	1800	6	5180581-1	Patent No. 5180581
16	265	9.5	2793	1	US-08-281-916-5	Sequence 5, Appl1
17	265	9.5	2793	1	US-08-460-725-7	Sequence 7, Appl1
18	180	6.4	6918	1	US-07-783-705A-13	Sequence 13, Appl1
19	175	6.2	1296	1	US-07-783-705A-8	Sequence 8, Appl1
20	172.5	6.2	1200	1	US-08-096-633A-19	Sequence 19, Appl
21	168.5	6.0	8051	2	US-08-576-626A-2	Sequence 2, Appl1
22	158	5.6	1245	1	US-09-337-913-2	Sequence 2, Appl1
23	158	5.6	1245	1	US-08-750-524-2	Sequence 2, Appl1
24	154.5	5.5	50937	4	US-09-428-517-1	Sequence 1, Appl1
25	150	5.4	1607	2	US-08-797-226-1	Sequence 1, Appl1
26	147	5.2	1627	3	US-09-106-464-1	Sequence 1, Appl1
27	143.5	5.1	1669	2	US-08-522-421-1	Sequence 1, Appl1
28	141	5.0	1731	2	US-08-466-583-1	Sequence 1, Appl1
29	141	5.0	1731	1	PCT-US95-07820-1	Sequence 1, Appl1
30	129.5	4.6	1332	1	US-08-660-765A-3	Sequence 3, Appl1
31	124	4.4	762	4	US-09-615-192A-218	Sequence 218, App
32	122	4.4	513	5	PCT-US92-00282-20	Sequence 20, Appl
33	120.5	4.3	3756	2	US-08-576-626A-1	Sequence 1, Appl1
34	119.5	4.3	330	4	US-09-615-192A-168	Sequence 168, App
35	119.5	4.3	1738	2	US-08-379-482A-2	Sequence 2, Appl1
36	115.5	4.1	80161	3	US-09-036-987A-1	Sequence 1, Appl1
37	115.5	4.1	80161	4	US-09-134-001C-1115	Sequence 1115, Ap
38	111.5	4.0	1176	4	US-08-975-316-32	Sequence 32, Appl
39	105.5	3.8	405	2	US-09-615-192A-32	Sequence 32, Appl
40	105.5	3.8	405	4	US-09-615-192A-114	Sequence 114, App
41	105.5	3.8	479	4	US-09-453-702B-57	Sequence 57, Appl
42	104	3.7	87563	4	US-08-961-527-44	Sequence 44, Appl
43	103	3.7	8657	4	US-09-024-020B-8	Sequence 8, Appl1
44	100	3.6	6826	3	US-09-425-043-8	Sequence 8, Appl1
45	100	3.6	6826	4		

## ALIGNMENTS

RESULT 1  
US-09-180-852-1  
Sequence 1, Application US/09180852  
Patent No. 6287834  
GENERAL INFORMATION:  
APPLICANT: BELANGER, Alain  
APPLICANT: HUM, Dean W.  
APPLICANT: BEAULIEU, Martin  
APPLICANT: LEVESQUE, Eric  
TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE  
FILE REFERENCE: 1259-449  
CURRENT APPLICATION NUMBER: US/09/180,852  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: PCT/CA97/00328  
EARLIER FILING DATE: 1997-05-16  
EARLIER APPLICATION NUMBER: US 08/649,319  
EARLIER FILING DATE: 1996-05-17  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2107  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52) .. (1644)  
US-09-180-852-1  
Alignment Scores:  
Pred. No.: 3.53e-198  
Score: 1732.00  
Percent Similarity: 75.47%  
Best Local Similarity: 61.51%  
Query Match: 61.81%  
Length: 2107  
Matches: 326  
Conservative: 74  
Mismatch: 112  
Indels: 18  
Gaps: 3

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US-09-784-340-2 (1-527) x US-09-180-852-1 (1-2107)
QY 9 ValPheLeuLeuGlnLeuPheCys---ValGlyCysGlyPheCysGlyLysValLeu 27
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Db 73 GCTCTTCCTGCTATGACAGTCAGTTGTTACTTACCTGCTGGAGAGTTGGAAAGTGTCTG 132
QY 28 ValTTPProCysAspMetSerHisTTPLeuAsnValLysValLLeuGlnLeuLeu 47
   |||||
Db 133 GCTGTGCCCAACAGATACAGCCATTGGATAAATATGAAACAACTCTGGAGACGTTGTT 192
QY 48 ValArgGlyHisGlnValThrValLeuThrHisSerLysProSerLeuLeaSPtyrArg 67
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Db 193 CAGAGGGGCTATGAGTGTATGTTGAGACATCTCGGCTTCTATTCTGTCAATGCCAGT 252
QY 68 LysProSerAlaLeuLysPheGlnValValHisMetProGlnAspArgThrGlnGlnAsn 87
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Db 253 AAATCATCTGCTATTAATAATTAGAACTTATCCATCATCTTAACTAAATAATGATTTGGAA 312
QY 88 GlnIlePheValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTrrpGlnSerVal 107
   |||||
Db 313 GATTTTATTATGAAATG-----TTGATATGATGAGCATATAGT 351
QY 108 IleLysLeuAsnAspPhePheValGlnIleArgGlyThrLeuLysMet----- 123
   |||||
Db 352 ATTTCAAAAATATCATTTTGTGCTATTTTTCACAACTACAAAGAAATGTGTGGAAATAT 411
QY 124 -----MetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLys 137
   |||||
Db 412 TCTGACTATATATTAAGCTCTGTGAAAGATGACAGTTTGAACAAGAACTATAGAAAAA 471
QY 138 LeuGlnGlnThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeu 157
   |||||
Db 472 CTACAAAGATCAAAATTTGATGTCCTCTGCGCAGATGCCCTTAATCCCTGTGTGAGCTG 531
QY 158 MetAlaGlnLeuAlaValProPheValLeuThrLeuArgLysSerValGlyLysAsn 177
   |||||
Db 532 CTGCTGAACTACTTAACATCCCTTCTGTACAGTCTCCGCTCTCTGTGTGGCTACACA 591
QY 178 MetGlnArgSerCysGlyLysLeuProAlaProLeuSerTyrValProValPrometThr 197
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Db 592 GTTAGAGAAATGATGAGGATTTCTGTCTCCCTCTCTATGATGATGATGATGATGATG 651
QY 198 GlyLeuThrAspArgMetThrPheLeuGlnLysValLysAsnSerMetLeuSerValLeu 217
   |||||
Db 652 GAATTAAGTGTCAAAATCATTTTCAATGAGAGATATAAAATATGATATATATCTTTAT 711
QY 218 PheHisPheTrrpIleGlnAspTyrAspTyrHisPheTrrpGlnGluPheTyrSerLysAla 237
   |||||
Db 712 TTTGACTTTTGGTTTCAAGCATATGATCTGAAGAAAGTGGACAGTTTATATGAGAGTT 771
QY 238 LeuGlyArgProThrThrLeuCysGlnThrValGlyLysAlaGlnIleTrrpLeuIleArg 257
   |||||
Db 772 CTAGAGAAAGCCACTACATTTATTTGAGAAATGGGGAAGCTGAATAATGTGCTCATTCGA 831
QY 258 ThrTyrTrrpAspPheGlnPheProGlnProTyrGlnProAsnPheGlnPheValGlyGly 277
   |||||
Db 832 ACCATATGGGATTTTGAATTTCTGCCCCATTTCTTACCAAAATGTGATTTTGTGGAGGA 891
QY 278 LeuHisCysLysProAlaLysAlaLeuProLysGlnMetGlnAsnPheValGlnSerSer 297
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Db 892 CTTCACTGTAACCAAGCCAAACCTTGCTAGAGAAATGAGAGATTTGTGAGAGCTCT 951
QY 298 GlyGlnAspGlyTyrLeuValAlaPheSerLeuGlnSerLeuPheGlnAsnValThrGlnGln 317
   |||||
Db 952 GGGAGAAATGATATGTGTGTGTCTGTGGGGTGCATGATATGATACATGTCAAGAAAGA 1011
QY 318 LysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValLeuTrrpArgTyr 337
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Db 1012 AGTGGCAACATGATTTTCATCAGCCCTTGCCAGATCCCAAAAGGTTCTATAGAGATTT 1071
QY 338 LysGlyLysLysProSerThrLeuGlyAlaAsnThrArgLeuTyrAspTrrpIleProGln 357
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Db 1072 GATGGCAGAGAACCAATACTTAGTTCACATCTGACATGATATAGTGTATACCCAG 1131
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Db 1132 AATGACCTTCTGTGCTATCCCAAAACCAAGCTTTTATATCATCTATGATGTGAAACCAATGCC 1191
QY 378 IleTyrGlnAlaIleTyrHisGlyValProMetValGlyValProIlePheGlyAspGln 397
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Db 1192 ATCTATAGGCGATCTCAACATGGATCCCTTATGTGTGGGCAATCCCTTGTGGGATCA 1251
QY 398 LeuAspAsnIleAlaHisMetLysAlaLysGlyAlaAlaValGlnIleAsnPheLysThr 417
   |||||
Db 1252 CATGATTAACATTTGCTACATGAAAGCCAAAGAGACACCTTCAGTGTGACATCAGGACC 1311
QY 418 MetThrSerGlnAspLeuLeuArgAlaLeuArgThrValIleThrAspSerSerTyrLys 437
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Db 1312 ATGTCAAATACAGATTTGCTCAATGATGAAAGCAGTCAATTAATGACCTATATATAA 1371
QY 438 GlnAsnAlaMetArgLeuSerArgIleHisHisAspGlnProValLysProLeuAspArg 457
   |||||
Db 1372 GAGATATCATGAATATATCAAGAAATTCATCATGATCAACCGGTGAAGCCCTGTGATGA 1431
QY 458 AlaValPheTrrpIleGlnPheValMetArgHisLysGlyAlaLysHisLeuArgSerAla 477
   |||||
Db 1432 GCAGCTTCTGATGATGATTTGTCATGCGCATTAAGAGCAAGCAACCTTGGGCTGCA 1491
QY 478 AlaHisAspLeuThrTrrpPheGlnHisTyrSerIleAspValIleGlyPheLeuLeuThr 497
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Db 1492 GCCCAACACTGACCTGATGATCCAGTACACACCTTTGGATGTGATAGCATTCCTGCTGCC 1551
QY 498 CysValAlaThrAlaIlePheLeuPheThrLysCysPheLeuPheSerCysGlnLysPhe 517
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Db 1552 TCGGTGGCAATGATATATATATGATACAAAATGTGCTGTGTTTGTTCGGAAGCTT 1611
QY 518 AsnLysThrArgLysIleGlnLysArgGln 527
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Db 1612 GCCAAACAGAAAGAAAGAAAGGAGT 1641

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RESULT 2
US-09-813-918-1
? Sequence 1, Application us/09813918
? Patent No. 6383789
? GENERAL INFORMATION:
? APPLICANT: WEBSTER, Marion et al.
? TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
? TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
? TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
? FILE REFERENCE: CL001175
? CURRENT APPLICATION NUMBER: US/09/813,918
? CURRENT FILING DATE: 2001-03-22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ. ID NO. 1
? LENGTH: 1413
? TYPE: DNA
? ORGANISM: Human
? US-09-813-918-1

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Alignment Scores:
Pred. No.: 2,21e-158 Length: 1413
Score: 1399.00 Matches: 277
Percent Similarity: 62.83% Conservative: 56
Best Local Similarity: 52.26% Mismatches: 103
Query Match: 49.93% Indels: 94
DB: 4 Gaps: 5

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US-09-784-340-2 (1-527) x US-09-813-918-1 (1-1413)
QY 9 ValPheLeuLeuGlnLeuPheCys---ValGlyCysGlyPheCysGlyLysValLeu 27
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Db 44 GTTCTCTGCTGATACATCTCAGTTGTTACTTATGCTCTGGAGCTGTGGAAGAGTCTG 103

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Alignment Scores:

Pred. No.:	9,31e-126	Length:	2336
Score:	1131.00	Matches:	234
Percent Similarity:	62.21%	Conservative:	87
Best Local Similarity:	45.35%	Mismatches:	185
Query Match:	40.36%	Indels:	10
DB:	5	Gaps:	6

US-09-784-340-2 (1-527) x PCT-US92-00282-1 (1-2336)

Oy	15	LeuPheCysVal-----GlyCysGlyPheCysGlyLysValLeuValTrpProCys	31
Db	46	CTGCTGTGTGTGGCGGGCCAGTGGTGTCCATGCTGGAGAAAGTACTGGATCCCAAGT	105
Oy	32	AspMetSerHisTrpLeuAsnValLysValIleuGluIuLeuValLeuValArgLysHis	51
Db	106	GATGCACACCCATGGCTGTAGATCTTGGGGCCATCCAGCAGCTGCAGCAGAGAGGACAT	165
Oy	52	GIuValTrpValLeuThrHisSerLysProSerLeuIleAspTrpArgLysProSerAla	71
Db	166	GAATAGATGGTGTCTTAGCA-----CTGACGCCCTGTTGTATCATCAAGACGAGGACA	216
Oy	72	Leu---LysPheGluValValHisMetProGluAspArgTrpGluLysGluIlePhe	90
Db	217	TTTTACACCTTGAAGAGCTACCTGTGTGCATTCCAAAGGAGAGGTGTGAAGAAGTCTTT	276
Oy	91	ValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTrpArgIleSerValIleLysLeu	110
Db	277	GTTACTCTGGGCAATAAGTTTGTGAGATGATTTCTTCCGACAGCGTGTGATCAAAAC	336
Oy	111	AsnAspPhePheValGluIleArgGlyTrpLeuLysMetCysGluSerPheIleTrp	130
Db	337	TACAGAAATAAAAAAGACGCTGCTATGCTTTGTCTGGCTGTGCCACTTACATGCAC	396
Oy	131	AsnGluTrpIleuMetLysLysLeuGluGluTrpHisAspValMetLeuIleAspPro	150
Db	397	AACAAGAGAGCTACGCTCCCTGCGAAGAGACGTTGTGATGCATAGCTGCAGCGACCT	456
Oy	151	ValIleProCysGlyAspLeuMetAlaGluIleuLeuAlaValProPheValLeuThrLeu	170
Db	457	TTTCCTTCGTGAGCGCCCATGCTGGTCCAGTACTGTCTGTGCCCATGTATTTCTCTTG	516
Oy	171	ArgIleSerValGlyLysAsnMetGluArgSerCysGlyLysIleuProAlaProLeuSer	190
Db	517	CAT---GCACGTGCCATGCAGCGCTGGAAATTTGAGGCTACCCGACCCCAACCATTTCTCC	573
Oy	191	TrpValProValProMetThrGlyLeuThrAspArgMetThrPheLeuGluAlaTrpValLys	210
Db	574	TACGTGCCAGGCGCTCTCTCTCTCATTCACATACATAGCATTTCTCTGCAGCGGGTAG	633
Oy	211	AsnSerMetLeuSerValLeuPheHisPheTrpIleGluAspTrpArgTrpHisPheTrp	230
Db	634	AACATGTCATTTGCCCTTTTACACAGAACTT---CTGTGCGACGATGGTTATTCGCCGTAT	690
Oy	231	GluGluPheTrpSerLysAlaLeuGlyLysArgProThrThrLeuCysGluTrpValGlyLys	250
Db	691	GCACCCCTTGCCTCAGATTCCTTCAGAGAGAGGTGACTGTCCAGGACCTATTAGAGCTCT	750
Oy	251	AlaGluIleTrpPheIleArgThrTrpTrpAspPheGluPheProGluProTrpGluPro	270
Db	751	GCATCTGTCTGGCTTTTGAAGTACCTTTTGAAGTATTCCTTAGGCCCATTCATGCC	810
Oy	271	AsnPheGluPheValGlyLysHisCysLysProAlaLysAlaLeuProLysGluMet	290
Db	811	AATATGGTTTTTGTGTGGGAATCACTGCTTCACCAAAATCCACTATGCCAGAGATT	870
Oy	291	GluAsnPheValGlnSerSerCylGluAspGlyIleValValPheSerLeuGlySerLeu	310
Db	871	GAAGCCTACATTAAATGCTTTCGGAGAACATGGAAATGTGGTTTTCTCTTGGGATCAATG	930
Oy	311	PheGluAsnValTrpGluGluLysAlaAsnIleAlaSerAlaLeuAlaGluIlePro	330
Db	931	GTCTCAGAAATTCAGAGAAAGAACTTTGGCAATTTGCTGTATGTTGGGAAATATCTCT	990

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QY 331 GlnyValLeuThrArgTyrLysGlyLysProSerThrLeuGlyAlaAsnThrArg 350
Db 991 CAGACAGCTGTCGTGGCGGTCACTGACGACCCAGCAGCATGATCTGGACACACAGCAT 1050
QY 351 LeuYrAspTrpIlePheProGlnAsnAspLeuLeuGlyHisProLysThrLysAlaPheIle 370
Db 1051 CTTGTTAAGTGGCTACCCCAAAACGATCTGTCTGGTGCACCCGATACACCCGCTTATC 1110
QY 371 ThrHisGlyMetAsnGlyIleTyrGluAlaIleTyrHisGlyValProMetValGly 390
Db 1111 ACCCATGCTGGTCCCATGCTGTTTATGAAGCATATGCAATGACGCGTCCATGGTGTG 1170
QY 391 ValProIlePheGlyAspGlnLeuAspAsnIleAlaHisMetLysAlaLysGlyAla 410
Db 1171 ATGCGCTGGTGGTGTATGATGCAATGCAATGCAAAAGCCATGAGACTTAAGGAGCTGA 1230
QY 411 ValGlnLeuAsnPheLysThrMetTrpSerGluAspLeuLeuAlaLeuArgThrVal 430
Db 1231 GTGACCCGATGTCTCGAATAGACTCTCGAAGATTGAAATAGTCTTAAAGCAGCTC 1290
QY 431 IleThrAspSerSerTyrLysGluAsnAlaMetArgLeuSerArgIleHisAspGln 450
Db 1291 ATCATGTACAAATGTACAAGAGAACATCAGCGCCTCCAGCGCTTCACAAAGAGCCG 1350
QY 451 ProValLysProLeuAspArgAlaValPheTrpIleGluPheValMetArgHisLysGly 470
Db 1351 CCGGTGGAGCCGCTGACACTGCGCGTGTCTGGGTGAGATTGTGATGACGACAAAGGC 1410
QY 471 AlaLysHisLeuArgSerAlaAlaHisAspLeuThrTrpPheGlnHisTyrSerIleAsp 490
Db 1411 GCGCACACACTGCGCCCGGACGACCAAGCAGCTCAGCTGTACAGACCATCTCTGTGAC 1470
QY 491 ValIleGlyPheLeuLeuThrCysValAlaIlePheLeuPheThrLysCysPhe 510
Db 1471 GGTATGGTTCCTCTGGCGCGTGTGCTGACAGTGGCTTATCACTTTAATGTTGCT 1530
QY 511 LeuPheSerCysGlnLys---PheAsnLysThrArgLysIleGluLys 525
Db 1531 GCTTATGCTACCGGAATGCTTGGGAAAAAAGGCGAGTTAAGAAA 1578

RESULT 4
PCT-US92-00282-2
Sequence 2, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OMENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944

```

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;       TELEX: 6714627 CUSH
;       INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 2339 base pairs
;       TYPE: NUCLEIC ACID
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;
PCT-0592-00282-2

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**Alignment Scores:**

Pred. No.:	3 12e118	Length:	2339
Score:	1068.50	Matches:	230
Percent Similarity:	57.56%	Conservative:	82
Best Local Similarity:	42.44%	Mismatches:	173
Query Match:	38.13%	Indels:	57
DB:	5	Gaps:	8

US-09-784-340-2 (1-527) x PCT-US92-00282-2 (1-2339)

QY	11	LeuLeuLeuGlnLeuPheCysValGlyCysGlyPheCysGlyLysValLeuValTyrPro	30
Db	46	CTGGCTGCTCCCTCCAGTGTCCACGCCCTGGGCTGAGATGGAAAGGCTGTGGTGCC	105
QY	31	CysAspMetSerHisThrPheAsnValLysValLLeuGluGluLeuLLeuValArgGly	50
Db	106	ACTATGGACACCCCTGGCTCAGATCGGGAGGCTTGGGGAGCTCATGCCAGAGGC	165
QY	51	HisGluValThrValLeuThr-----HisLysPro-----	61
Db	166	CACCAAGGGGTGGTCTCACCCACAGAGGTGATATGCACATCAAGAAGAAATTTTC	225
QY	62	SerLeuLeaSPyrArgLysProSerAlaLeuLys-----	73
Db	226	ACCCGACAGCCTATGGCTGTTCATGGACCCAGAAAGAAATTGATCGCGTTACGCTGGC	285
QY	74	-----PheGluValValHisMetProGlnAspArgThrGluGluAsnGlu	88
Db	286	TACACTCAAGGCTTCTTGGAAACAGAACATCTCTGAGAAGATATCTCAAGATAGCA	345
QY	89	IlePheValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTrpGlnSerValIle	108
Db	346	ATTATGAACATGATCTTTG-----	366
QY	109	LysLeuAsnAspPhePheValGluIleArgGlyThrLeuLysMetMetCysGluSerPhe	128
Db	367	-----GCCCTCATAGCTGTGTGTGGAGCTA	393
QY	129	IleTyrAsnGlnThrLeuMetLysLysLeuGlnGlnLThrAsnTyrAspValMetLeuIle	148
Db	394	CTGCATATATGAGGGCCGATCAGACACCTGAATGCTACTTCTTGATGTGGTTTACAA	453
QY	149	AspProValIleProCysGlyAspLeuMetAlaGluLeuLeuAlaValProPheValLeu	168
Db	454	GACCCGTTAATCTCTCGGGGGCGGTGCTGGCTAAGTACCTGTGCATCTCGCTGT	513
QY	169	ThrLeuArgIleSerValGlyLysMetGluArgSerCysGlyLysLeuProAlaPro	188
Db	514	TTTTGGAGGTAC--ATTTCATGTGACTTGAAGGACACAGTGTCCAAATCT	570
QY	189	LeuSerThrValProValPrometThrGlyLeuThrAspArgMetThrPheLeuGluArg	208
Db	571	TCTCTCATATATCTCTAAGTACTACAGCAACAAATTCACACATGACATTCCTGCAAAAG	630
QY	209	ValLysAsnSerMet-----LeuSerValLeuPheHisPheTrpIleGlnAsp	224
Db	631	GTCAGAAACATGCTCTACCCCTGTGCTCTACACTTGGCCATCTTTTCTGCCCT	690
QY	225	TyrAspTyrHisPheTrpGluGluPheTyrSerLysLeuAlaGluArgProThrThrLeu	244
Db	691	TAT-----GCAGTCTTGGCTGTGACCTTTTTCAGAGAGAGGTGTGATG	735
QY	245	CysGluThrValGlyLysAlaGluIleTrpLeuIleArgThrTyrTrpAspPheGluPhe	264

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Db      736 GTGATCTTGTGCACGTATGATGATCCGTTGGCTTTCCGAGGGAGCACTTGTGATGGACATAC 795
      265 ProGlnProtyrGlnProAsnPhneGluPhnValGlyGlyLeuHisCysLysProAlaLys 284
      796 CCCAGGCCGATCATGCCCAACATGCTCTTATATGGGGGATCAACTGTGCCAACGGGAG 855
      285 AlaLeuProLysGluMetGluAsnPhneValGlnSerSerGlyLyspGlyLeuVal 304
      856 CCACATATCTACGGAAATTGGAAGCCCTACATTAACTCTTCGGAGAACATGGAAATTGGTT 915
      305 PheSerLeuGlySerLeuPheGlnAsnValThrGluGlyLysAlaAsnIleIleAlaSer 324
      916 TTTCTCTTTGGGATCAATAGTGTCTCAGAAATTCCAGACAGAAAGACTGTGGCATTTGCTAT 975
      325 AlaLeuAlaGlnIleProGlnLysValLeuTrpArgTyrGlyGlyLysLysProSerThr 344
      976 GCTTTGGGCAAAATCCCTCCAGACAGTCTGTGGCGGTACACTGGAAACCCGACATCGAAT 1035
      345 LeuGlyAlaAsnThrArgLeuTyrAspTrpIleProGlnAsnAspLeuGlyHisPro 364
      1036 CTTCGGAACAACACAGAACTGTGTTAAATGGCTACCCCAAAAGCATCTGCTGTCCACCCG 1095
      365 LysThrLysAlaPheIleThrHisGlyGlyMetAsnGlyIleTyrGlnAlaIleTyrHis 384
      1096 ATGACCCGCTGCTTTATTCACCCATGCTGGTCTCCCATGCGTTTATGAAAGCATATGACAT 1155
      385 GlyValProMetValGlyValProIlePheGlyAspGluLeuAspAsnIleAlaHisMet 404
      1156 GCGCTTCCCATGTGATGATGATGCCCTTGTGTGGTATCAATGACATGCAATGCCAAGCGCATG 1215
      405 LysAlaLysGlyAlaAlaValGluIleAsnPhneLysThrMetHisSerGluAspLeu 424
      1216 GAGACTAAGGAGAGCTGGAGTGAACCTCGAATGTTCTCGGAATGACTTCTGAACATTTACAA 1275
      425 ArgAlaLeuArgThrValIleThrAspSerSerTyrLysGluAsnAlaMetArgLeuSer 444
      1276 AATGCTCTAAAGAGCATCATCAATGACAAAGATTACAGAGAGCATCAGGCGCCTCTCC 1335
      445 ArgIleHisAspGlnProValLysProLeuAspArgAlaValPheTrpIleLeuIlePhe 464
      1336 AGCCTTCACAGAGACCGCCGCGGAGACCCCTGTGACTGCGGTGTGGGTGGAGATT 1395
      465 ValMetArgHisLysGlyAlaLysHisLysLeuArgSerAlaAlaHisAspLeuThrTrpPhe 484
      1396 GTGATGAGCACAAAGGGCGGCCACACACTGCGCCCGGCAACCCAGACCTCACCTGGATAC 1455
      485 GlnHisTyrSerIleAspValIleGlyPheLeuLeuThrCysValAlaThrAlaIlePhe 504
      1456 CAGTAACATCTCTTGGAGACGATTTGGTTCTTGTGGCGGTGCTGACATGGCCCTTC 1515
      505 LeuPheThrLysCysPheLeuPheSerCysGlnLys--PheAsnLysThrArgLysIle 523
      1516 ATCACTTTAAATATGTGTGCTTATGCTACCGGAATGCTTGGGAAAAAAAGCGCAATT 1575
      524 GluLys 525
      1576 AAGAAA 1581

RESULT 5
; Sequence 21, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Monmach, Rodon
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370, 838
; CURRENT FILING DATE: 1999-08-09

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: EARLIER APPLICATION NUMBER: US 09/285,323
: EARLIER FILING DATE: 1999-04-02
: NUMBER OF SEQ ID NOS: 289
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 21
: LENGTH: 391
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-370-838-21

Alignment Scores:
Pred. NO.: 5,77e-38 Length: 391
Score: 391.00 Matches: 75
Percent Similarity: 72.09% Conservative: 18
Best Local Similarity: 58.14% Mismatches: 36
Query Match: 13.95% Indels: 0
DB: Gaps: 0

US-09-784-340-2 (1-527) x US-09-370-838-21 (1-391)
QY 301 G1Y1LeVal1Val1PheSerLeuGlySerLeuPheGlnAsnVal1ThrGluGluYsAlaAsn 3200
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 GGAATTGCTGCTTTCTCTCTTGGGATCAATGGCTCCAGAAATATCCAGAGAGAAAGACTGTG 62
QY 321 IleIleAlaSerAlaLeuAlaGlu1IleProGlnYsValLeuTrpArgTyrYrYsGlyLys 3400
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 GCGATTGCTGATGCTTTGGGCGAAAATCCCTGAGACAGTCCGTGGGCGGTACACTGGACC 1220
QY 341 LysProSerThrLeuGlyAlaAsnThrArgLeuYrAspTrpIleProGlnAsnAspLeu 3600
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 CGACCATGGAATCTTGGCAACAACACGATACTGTTGACGTGCTACACCCCAAAAGCATCTG 1820
QY 361 LeuGlyHisProLysThrYsAlaPheIleThrHisGlyGlyMetAsnGlyIleYrGlu 3800
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 CTGGTCACCAATGACCGCGCTTATCATCCCATGCTAGTCCCATGTCAGTGGTAAATGAA 2420
QY 381 AlaIleYrHisGlyValProMetValGlyAlaProIlePheGlyAspGlnLeuAspAsn 4000
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 AGCATATCAATGACGCTCCCATGGTGTATGATACCTTATTTGGTGTATCAGATGGACAT 3020
QY 401 IleAlaHisMetLysAlaYsGlyValAlaValGluIleAsnPheLysThrMetThrSer 4200
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 GCAAAAGCCGACGAGGAGACTCAAGGAGCTGGAGCTGACCCCTGAATGTTCTGAGATGACTTCT 3620
QY 421 GluAspLeuLeuArgAlaLeuArgThr 429
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 363 GAAGATCTAGAAGATGCTCTGAAGAGC 389

RESULT 6
PCT-US92-00282-18
: Sequence 18, Application PC/TUS9200282
: GENERAL INFORMATION:
: APPLICANT: OWENS, IDA S.
: APPLICANT: RITTER, JOSEPH K.
: TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
: TITLE OF INVENTION: THEREIN.
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: CUSHMAN DARBY & CUSHMAN
: STREET: 1615 L STREET, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20036-5601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/00282
: FILING DATE: 19920110
: CLASSIFICATION: 435

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: ATTORNEY/AGENT INFORMATION:
: NAME: SCOTT, WATSON T.
: REGISTRATION NUMBER: 26581
: REFERENCE/DOCKET NUMBER: 91532-PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-861-3000
: TELEFAX: 202-822-0944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1190 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: PCT-US92-00282-18

Alignment Scores:
Pred. No.: 1,54e-35 length: 1190
Score: 377.50 Matches: 92
Percent Similarity: 52.96% Conservative: 51
Best Local Similarity: 34.07% Mismatches: 118
Query Match: 13.47% Indels: 9
DB: 5 gaps: 5

US-09-784-340-2 (1-527) x PCT-US92-00282-18 (1-1190)
QY 15 LeupheycysVal-----GlycysgLyphcysgLylysValLeuValTrrpProcys 31
    ||| |||||
Db 130 CTGCGTGTGTGCGTGGCGCCAGTGGTGTGCCATCTGGGAAGATACGTGTGATCCCGAGTG 169
    ||| |||||

QY 32 AspmetSerHisTrrpLeuAsnVallysValIleLeuglucgluLeuIleValArgglyHis 51
    ||| |||||
Db 190 GATGGCACCCCACTGGCTGACATCTTGCGGCGCATCCAGCAGCTGCAGCAGAGGGGCAAT 249
    ||| |||||

QY 52 GluValIthrValleuThrHisSerLysProSerleuIleAspTryrArgLysProserAla 71
    ||| |||||
Db 250 GAAATATGTTGTCCTTAGCA-----CTTACGCCCTCGTTTGCATCAGACGAGCAGCA 300
    ||| |||||

QY 72 Leu---LysPhegluValValHisMePProgluAsnArgTrrpGluIuAsnGluIlePhe 90
    ||| |||
Db 301 TTTTACACCTTGAGAGACTACCCCTGTGCAATCCAAAGGAGAGATGGAAGAGCTCTTT 360
    ||| |||

QY 91 ValAspLeuAlaLeuAsnValLeuProgluLeuSerThrTrrpGlnSerValIleLysLeu 110
    ||| |||
Db 361 GTTAGTCTCGGGCATAAATGTTTGGAGATGATCTTCTCCGACGCTGATCAAAACA 420
    ||| |||

QY 111 AsnAspPhePheValGluIleArgglyIthrLeuLysMetLysGlnSerPheIleTyr 130
    ||| |||
Db 421 TACAAGAAATATAAAAGAGACTGTCTATGCTTTTGTCTGGCTTTCCACTTACGTGCAC 480
    ||| |||

QY 131 AsnGlnThrLeuMetLysLysLeuGlnGlnIuThrAsnTryAspValMetLeuIleAspPro 150
    ||| |||
Db 481 AACAGAGAGCTCATGGCCCTCCCTGCGAAGACGACTTTGATGTCAATCGTCGAGGACCT 540
    ||| |||

QY 151 ValIleProCysgLyAspLeuMetalGluLeuLeuAlaValPropheValIleuThrLeu 170
    ||| |||
Db 541 TTCCTTCTCGAGCCCATCGTGGTGGCCAGTACCTGTCCTGGCCACTGATTTCTTCTTG 600
    ||| |||

QY 171 ArgIleSerValGlyglyAsnMetGluArgSerCysgLyLysLeuProAlaProLeuSer 190
    ||| |||
Db 601 CAT---GCACAGCCCATGCGAGCCTGGAATTTGAGGCTACCCAGCAGCCCAACCCATTCTC 657
    ||| |||

QY 191 TyrValProValProMetThrGlyLeuThrAspArgMetThrPheLeuGluIuArgValLys 210
    ||| |||
Db 658 TACGGTCCAGAGCCCTCTCTCTTCATTCACATACATGACATTCCTGCGACGGGGTAAG 717
    ||| |||

QY 211 AsnSerMetLeuSerValLeuPheHisPheThrIleGlnAspTryrAspTryrHisPheTrrp 230
    ||| |||
Db 718 AACATGCTCATTTGCCCTTTTTCACAGACTT---CTGTGCGACAGTGGTTTATCCCGCTAT 774
    ||| |||

QY 231 GluIuPheTyrSerLysAlaLeuGluIuArgProThrThrThrLysCysgLyuThrValGlyLys 250
    ||| |||

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Db 310 ATCAAAACAAGAAATTTTTCACCCCTGACACCAACTATGCCATTTCATGAGCCAGATGAA 369
Oy 84 ThrGlu-----GluangluileValasp 92
Db 370 TTTGATGCCCTTGTCGTGGGCGACACACACACTGACTGATTTGAACAGCAATTTT----- 423
Oy 93 LeuAlaLeuAsnValLeuProGlyLeuSerThrTrpGlnSerValIleLysLeuAsnsp 112
Db 424 -----CTGAAAGCATTTTCTTAAAGATGATGCAATTTTGGAAA---AATTCA 465
Oy 113 PhePheValIGluIleArgGlyThrLeuLysMetMetCysGluSerPheIleIleTyrAsnGln 132
Db 466 TCTTTGGCTTTTCATAGCTCT-----TGTGTGAGCTACTGACCTAAAGAG 510
Oy 133 ThrLeuMetLysLysLeuGlnIGluThrAsnTyrAspValMetLeuIleAspProValIle 152
Db 511 GCCCGATCAGGACACCTGAATGCTACTTCTCTGCATGTGGTTTAATAGACCAATTTAC 570
Oy 153 ProCysGlyAspLeuMetAlaGluLeuLeuAlaValAProPheValLeuThrLeuArgIle 172
Db 571 CTCGTGTGGGCGAGTGTGCTGAATGACTATCAATCAATCTGCTGTGTTTTTTTGAGG--- 627
Oy 173 SerValIGlyLysAsnMetGluArgSerCysGlyLysLeuProAlaProLeuSerTyrVal 192
Db 628 AACATCTCCATGTGATTTAGACTTTAAGGGCGACACAGCTGCCAAATCTCTCCTCATATT 687
Oy 193 ProValAPrometThrGlyLeuThrAspArgMetThrPheLeuGluIleArgValLysAsnSer 212
Db 688 CCTAAGTACTAGACCAATTCAGACCATGACATTCCTCTGCAAGGGTCAAGAAACATG 747
Oy 213 Met-----LeuSerValLeuPheHisPheThrIleGlnAspTyrAspTyrHis 228
Db 748 CTCATCCCTGTGGCGCTGCTCCTACTCTTGCCATCTCTTCTGTGCTCTTAT----- 798
Oy 229 PheTrpGluIleuPheTyrSerLysAlaLeuGlyArgProThrThrIleCysGluThrVal 248
Db 799 -----GCAGACCTTGCCCTCGACCTTTTTCAGAGGGAGGTGATGAGTGGATCTTCTC 852
Oy 249 GlyLysAlaGluIleTrpLeuIleArgThrTyrTrpAspPheGluPheProGlnProTyr 268
Db 853 AGCCATGCACTGTGTGTGCTTCCGAGGGAGCTTTGTGATGATTAACCCAGGCGCATC 912
Oy 269 GlnProAsnPheGluPheValIGlyLysCysLysProAlaLysAlaLeuProLys 288
Db 913 ATGCCACACATGGTCTTCATTTGGGGGCGATCAACGTGCCAAGGAAGCAGCATATCTCAG 972
Oy 289 ---GluMetGluAsnPheValGlnSer 296
Db 973 GTCGGTGTTCGTGCTTCATTCACATCA 999

RESULT 8
PCT-US92-00282-10
Sequence 10, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
TITLE OF INVENTION: THEREIN.
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282

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FILING DATE: 19920110  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SCOTT, WATSON T.  
 REGISTRATION NUMBER: 26581  
 REFERENCE/DOCKET NUMBER: 91532-PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 TELEX: 6714627 CUSH  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1008 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 PCT-US92-00282-10

Alignment Scores:  
 Pred. No.: 1.95e-28 Length: 1008  
 Score: 317.50 Matches: 91  
 Percent Similarity: 46.51% Conservative: 49  
 Best Local Similarity: 30.23% Mismatches: 128  
 Query Match: 11.33% Indels: 33  
 Gaps: 7

US-09-784-340-2 (1-527) x PCT-US92-00282-10 (1-1008)

QY 11 LeuLeuLeuGlnLeuPheCysValAlGlyCysGlyPheCysGlyValLeuValLeuValTrpPro 30  
 Db 157 CTGCTGCTTCTCCTCAGTGTCCAGCCCTGGGCTGAGAGTGGGAAGTGTGCTGCTGCC 216  
 QY 31 CysAspMetSerHisTrpLeuAsnValLeuValLeuGlnGluLeuValLeuValArgGly 50  
 Db 217 ACTGATGGCAGCATCTGCTGCTGATGGGAGGCGCTTGGGAGCTCATGCGAGAGGC 276  
 QY 51 HisGluValThrValLeuThrHisSerLysProSerLeuLeuAspTyrArgLysProSer 70  
 Db 277 CACGAGGTGGTGGTCTCCACCTGGAGGTGAATATGATCACTCAAGAAGACACTTTTTC 336  
 QY 71 AlaLeuLysPheGluValValHisMetProGlnAspArgThrGluLysAsnGluLeuPhe 90  
 Db 337 ACCGTGACACGATGCCATTTTCATGAGACCGAGACGAA----- 375  
 QY 91 ValAspLeuAlaLeuAsnValLeuProGlyLeuSerThrTrpGlnSerValLeuLysLeu 110  
 Db 376 TTGTATCGCCCTTTTG-----CTGGGTCAACACTCAATCGTTCTTGAACA 420  
 QY 111 AsnAspPhePheValGluLeuArgGlyThrLeuLysMetMet----- 124  
 Db 421 GAACATCTTCTGTGAATAATTTTCTAGAGAATGCAATATGATGCTTTGATC 480  
 QY 125 -----CysGluSerPheLeuTyrAsnGlnThrLeuMetLysLysLeuGlnGlu 140  
 Db 481 ATACATAGTCTTGTGGAGTACTGATGAATAGGCCCTGATGAGGACCTGCTGCT 540  
 QY 141 ThrAsnTyrAspValMetLeuLeuLeuAspProValIleProCysGlyAspLeuMetAlaGlu 160  
 Db 541 ACTTCCTTGTATGTGTCTTACAGACCCCTTTCACCTTGCCGCGGCTGGCTGCTAG 600  
 QY 161 LeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGluArg 180  
 Db 601 TACCTGTGATCTCTGCTGTGTTTCTTGAGG---AACATTCAGATGATTTAGACTTT 657  
 QY 181 SerCysGlyLysLeuProAlaProLeuSerTyrValProValProMetThrArgLysLeuThr 200  
 Db 658 AAGGACACACAGTGTCCAAACCCCTTCTCTATATCTCTGATTTACTTAAGACCAATCA 717  
 QY 201 AsparGlyMetThrPheLeuGluArgValLysAsnSerMet-----LeuSerVal 216  
 Db 718 GACCACTGACATCTCTGCAAAAGGCTCAAGACATGCTCTACCTCTGCCCTGCTCTAC 777

QY 217 LeuPheHisPheTrpIleGlnAspTyrAspTyrHisPheTrpGlnGluPheTyrSerLys 236  
 Db 778 CTGTCATGCTGCTGTTCTGCTCTTAT-----GCAAGCCTTGCTCTGAG 822  
 QY 237 AlaLeuGlyArgProThrThrLeuCysGluThrValGlyLysAlaGluIleTrpLeuIle 256  
 Db 823 CTTTTCAGAGACAGAGGTGTGAGTGTGATCTGTACAGCATGATCTGCTGCTGCTTC 882  
 QY 257 ArgThrTyrTrpAspPheGluPheProGlnProTyrLysProAsnPheGluPheValGly 276  
 Db 883 CGAGGAGAGTTGTGATGATTTACCGAGCCGATCATGCCCAACATGCTCTTATTTGGG 942  
 QY 277 GlyLeuHisCysLysProAlaLysAlaLeuProLysGlu---MetGluAsnPheValGln 295  
 Db 943 GCATCAACTGTGCCAAGGAGGACCATATCTCAGTGTGATGCTGCTTATTCCTCA 1002  
 QY 296 Ser 296  
 Db 1003 TCA 1005

# RESULT 9

PCT-US92-00282-14  
 Sequence 14, Application PC/TUS9200282  
 GENERAL INFORMATION:  
 APPLICANT: OWENS, IDA S.  
 APPLICANT: RITTER, JOSEPH K.  
 TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION  
 TITLE OF INVENTION: THEREIN.  
 NUMBER OF SEQUENCES: 40  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DARB & CUSHMAN  
 STREET: 1615 L STREET, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20036-5601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/00282  
 FILING DATE: 19920110

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SCOTT, WATSON T.  
 REGISTRATION NUMBER: 26581  
 REFERENCE/DOCKET NUMBER: 91532-PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 TELEX: 6714627 CUSH  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1066 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 PCT-US92-00282-14

Alignment Scores:  
 Pred. No.: 6.3e-26 Length: 1066  
 Score: 297.00 Matches: 87  
 Percent Similarity: 47.35% Conservative: 56  
 Best Local Similarity: 28.81% Mismatches: 124  
 Query Match: 10.60% Indels: 36  
 Gaps: 7

US-09-784-340-2 (1-527) x PCT-US92-00282-14 (1-1066)

QY 11 LeuLeuLeuGlnLeuPheCysValAlGlyCysGlyPheCysGlyValLeuValLeuValTrpPro 30



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Db 176 CTGCTGCTTCCTCCAGTGTCCAGCCCTGGCGTGAAGAGGAAAGTGTGTGTGCTGCC 235
Qy 31 CysAspMetSerHisThrLeuAsnValIleLeuGluGluLeuIleValArgGly 50
Db 236 ATTCATGCGACGCTGCTCAAGCATGGCGGAGGCTTTCGGGAGCTCCATCCAGAGAGC 295
Qy 51 HisGluValThrValLeuThrHisSerLysProSerLeuIleAspTyrArgLysProSer 70
Db 236 CACCGAGGAGTGTGCTCTCAACCCCAAGAGTGAATATGCATCAAGAAGACACTTTTTC 355
Qy 71 AlaLeuLysPheGluValValHisMetProGlnAspArgTyrGlu----- 85
Db 356 ACCGTGACCAACCTATGCTATTCGTGAGACCCAGATGAATTGATGGCATGTGCTGGGC 415
Qy 86 -----GluAsnGluIlePheValAspLeuAlaLeuAsnValLeuPro 99
Db 416 CACACTCAACTGTACTTGAACACAGACATTTTTCGAAG----- 454
Qy 100 GlyLeuSerThrTyrGlnSerValIleLysLeuAsnAspPheValGluIleArgGly 119
Db 455 -----AAATTTTTCAGAAAGTATGSCAATGTTGAACAATATGCTTTG----- 496
Qy 120 ThrLeuLysMetMetCysGlnSerPheIleTyrAsnGlnThrLeuMetLysLysLeuGln 139
Db 497 GTCTATCATAGAGTCTTGTGTGGAGCTACTACATATATGAGCCCTGATCAGCAGCACTGAAT 556
Qy 140 GluThrAsnTyrAspValMetLeuIleAspProValIleProCysGlyAspLeuMetAla 159
Db 557 GCTACTTCTCTTGAGTGTGTTTAAACACCCCGTTAACCTCTCTGCGCGGCACTGCTGGCT 616
Qy 160 GluLeuLeuAlaValProPheValLeuThrLeuArgIleSerValGlyLysAsnMetGlu 179
Db 617 AAGTACCTGCTGCATCTCTACTGCTGTTTTTTTGGAGC---AACATTCACATGCTATTTAGC 673
Qy 180 ArgSerCysGlyLysLeuProLysLeuProLeuSerTyrValProValProMetThrGlyLeu 199
Db 674 TTTAAGGCGACACAGCTGTCCAAAACCTTCCTCTATATTCCTAGATTACTACAAACCAAT 733
Qy 200 ThrAspArgMetThrPheLeuGluArgValLysAsnSerMet-----LeuSer 215
Db 734 TCAGACCCACATGACATTCATCAAGAGGTCAGAACATGCTCTCTGCGCCCTGTGCC 793
Qy 216 ValLeuPheHisPheThrIleGlnAspTyrAspTyrHisPheTyrGluIlePheTyrSer 235
Db 794 TACATTTTGCATGCTTTTCTGCTCTTAT-----GCCAGCCTTGCCTCT 838
Qy 236 LysAlaLeuGluArgProThrThrLeuCysGluThrValGlyLysAlaGluIleThrLeu 255
Db 839 GAGCTTTTTCAGAGAGAGAGTGTCACTGATTCATTCAGATCAGCATGCTGTGTGGCTG 898
Qy 256 IleArgThrTyrTyrAspPheGluIlePheProGlnProTyrGlnProAsnPheGluIleVal 275
Db 899 TTCCAGGAGGACTTGTGTGATGATACCCAGGCAATCATCCCAATCATGTGCTTCAT 958
Qy 276 GlyGlyLeuHisCysLysProAlaLysAlaLeuProLysGlu---MetGluAsnPheVal 294
Db 959 GG-GGATCAACTGTGCCAACAGAGACCATATCTCAGGCTGTGATTGTGTGCTTCAATC 1017
Qy 295 GlnSer 296
Db 1018 CAATCA 1023

```

```

ADDRESS: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00282
FILING DATE: 19920110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US92-00282-22

Alignment Scores:
Pred. No.: 6.04e-25 Length: 783
Score: 287.00 Matches: 63
Percent Similarity: 38.89% Conservative: 14
Best Local Similarity: 31.82% Mismatches: 27
Query Match: 10.24% Indels: 94
Gaps: 1

US-09-784-340-2 (1-527) x PCT-US92-00282-22 (1-783)
Qy 330 ProGlnValLeuThrPArgTyrLysGlyLysLysProSerThrLeuGlyAlaAsnThr 349
Db 93 CCTCTCCAGGCTCTGTGGCGGTACCTGGAACCGACCATGGAATCTTGCGAACAACAG 152
Qy 350 ArgLeuTyrAspTyrIleProGlnAsnAspLeu----- 361
Db 153 ATACTGTGTAAGTGTGCTACCCCAAAAGCATCTGCTGTGTATGTTGGCGGATGGATGTA 212
Qy 361 ----- 361
Db 213 TAGGTCAACACGAGGTCAAAATTAAGAAATGGCTTAACACAGCTATTTAAAGATGT 272
Qy 361 ----- 361
Db 273 TGAGCTGAATAATTAATGGAACATATCTACATTCCTTTTATCTAGTGGGATATCTC 332
Qy 361 ----- 361
Db 333 AACCCACATTTTCTCTGCAAAATTTCTGCAAGGGCATGTGAGTAACACTGAGTCTTTGGA 392
Qy 361 ----- 361
Db 393 GTGTTTTCAGAACCTAGATGTGTCCAGCTGTGAACCTCAGAGATTAACCTCAGACATCC 452
Qy 362 -----GlyHisProLysThrLysAlaPheIleThrHisGlyGlyMet 375
Db 453 TCCCTATTTCGATCTCAGGTACCCGATGACCCGTGCTTTATTCATCCCATGCTGTGGTCC 512
Qy 376 AsnGlyIleTyrGluAlaIleTyrHisGlyValProMetValGlyValProIlePheGly 395
Db 513 CATGCTTTTATGAAGAAGATATGCAATGCGCTTCCCATGATGATGATGATGATGATGATG 572

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Oy	134	umelLysylsLeuclnGluThrAsn-----TyrAspValMetLeuIleAspProValI	152
Db	685	TTGACGAAATATGATGCAAAATCAAAAGTCTTTGATTTGGTGCACCGAAGCTTCT	744
Oy	152	eProCysGlyAspLeuMetIaGluLeuLeuAla---ValProPheValLeuThrLeuAr	171
Db	745	AGATTATCCCTGGTGTGTTTCCGATTTGTTGGCCGATGTCCT-----GTCAATACA	795
Oy	171	gIleSerValGlyLysAsnMetGluArgSerCysGlyLeuProValProIaProLeuSerTy	191
Db	796	AATTTCGTCGGGTACACGCTTTGGCGGCAAAATTTTGAGACAAATGGAGACC--GTAGAGCG	852
Oy	191	rValProValProMetThrGlyLeu-----	199
Db	853	ACATCCCATTTACTATCCAAATTTGGTGGCCCAACAAATTTCAAAATTTAAACGTTGGGA	912
Oy	200	-----ThrAspArgMetThrPheLeuGlu-----ArgValLysAs	211
Db	913	GATATATACGGAATCTATACAGACCTGGTCTGTACTTTGGAAATTTGCTCGTTTGGCGGA	972
Oy	211	nSerMetLeuSerValLeuPheHisPheTrpIleGlnAspTyArgSpTyHisPheTrpG1	231
Db	973	CGAACAAACATAAATGCTTGGCCAT-----	997
Oy	231	uGluPheTySerLysAlaLeuGlyArgProThrThrLeuCysGlyThrVal--GlyLy	250
Db	998	-----CAATTCGACCAACAAACGCCACCGCCAGTGAAGACATCGACACAGC	1041
Oy	250	sAlaGluuIleTrpLeuLeuArgThrTyrrTrpAspPheGluPheProGlnProTyGlnPr	270
Db	1042	CGTTCAATTAATGTTTGTGTGAATCGCATCCGCTGTTTGATTAATACAGACCGATCCGCC	1101
Oy	270	oAsnPheGluPheValGlyLysLeuHisCysLysProAlaLysAlaLeuProLysGluMe	290
Db	1102	GAGGTACAAATATTGGGAGGTCTACATCTTGATTCGAACAAATGATGTGACGAACACGA	1161
Oy	290	tGlu-----AsnPheValGln-----SerSerGlyLysAspGlyIleValIph	305
Db	1162	AACGATGACACTAATATTGGATGCAATTTTAATTAATATCTACAAACGGGTGGTGCAGT	1221
Oy	305	eSerLeuGlySer-----LeuPheGlnAsnVa	314
Db	1222	GAGTTCGGATACGCTTAATACAGCTTTCACAGATGACGACGAGATTTCTGTTGGAATTTAT	1281
Oy	314	1ThrGluGluLysAlaAsnIleIleAlaSerAlaLeuAlaGlnIleProGlnLysValIe	334
Db	1282	AACA-----GCTTCAACAGCATTAACCTTAATATATT	1314
Oy	334	uTrpArgTyLysGly--LysLysProSerThrIleuGlyAlaAsnThrArgLeuTyAs	353
Db	1315	GTGGAAACACCGATGATGCCATCGCAACGACATGCTGTAAATAATGGTTGTACACAAC	1374
Oy	353	pTrpIleArgProGlnAsnAspLeuLeuGlnHisProLysThrLysAlaPheIleThrHisG1	373
Db	1375	TTGGCTGCGCAACACCATATATTGAACACACAAATGATGATGTCATTGTTGTTGATCAAG	1434
Oy	373	yG1MetAsnGlyLysTyArgLysAlaIleTyrrHisGlyValPrometValGlyValProI1	393
Db	1435	CGGATCGAGTCAACGAGGACGACGATCGACGCTTGTGACACATATGGAAATCCGCTT	1494
Oy	393	ePheGlyAspGlnLeuAspAsnIleAlaHisMetLysAlaLysGlyAlaAlaValaGluI1	413
Db	1495	TATGAGCGGACACCAATACATACCAATAAATTCGAAAGAACATCGGAATGGACGACACCT	1554
Oy	413	eAsnPheLysThrMetThrSerGluAspLeuLeuAlaGlyAlaLeuAla-----ThrValI1	431
Db	1555	CGATCCCGTAACTGCTCAACGATATTTTGGTGTGCTGCGCTTTAGATGTGACCGGTAA	1614
Oy	431	eThrAspSerSerTyLysGlyLysAsnAlaMetArgLeuSerArgGluIleHisAspG1Pr	451
Db	1615	CACAAAGAGTGCCTACACACATATATTAAGCATTTGAATCGTCCACATTAATTATGACAC	1674
Oy	451	oValLysProLeuAspArgAlaValaPheTrpIleGluPheValMetArgHisLysGlyAl1	471

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Db      1675  ACGGAACCTTATGAAAAAGGCCATCTGTCACAGAACATGTAATGATGTAATAA 173
Oy      471  alyshisLeuArgerSerLiaIaHisAspLeuThrTrpPheGlnHisTyrSerLeu 491
Db      1735  TCCCATTTTAAAGAAAGAGGCCGCCCAACGATGCTATGACAAATATTATATGAGTAT 179
Oy      491  lIleGlyPheLeuLeuThr 497
Db      1795  CATGCTTCCTGTTATTAACG 1813

RESULT 13
PCT-US92-00282-8
; Sequence 8, Application PC/TUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; APPLICANT: RITTER, JOSEPH R.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; TITLE OF INVENTION: THEREIN.
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, MATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1219 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US92-00282-8

Alignment Scores:
Pred. No.:          7e-23          Length:          1219
Score:              272.50         Matches:          98
Percent Similarity: 46.67%         Conservative:    70
Best Local Similarity: 27.22%      Mismatches:     138
Query Match:        9.73%          Indels:          56
DB:                 5              Gaps:             10

US-09-784-340-2 (1-527) x PCT-US92-00282-8 (1-1219)

Oy      6  SerialLeuValPheLeuLeuLeuGlnLeuPheCysValGlyCysGlyPheCysGlyLys 25
Db      230  GCAGGGGCTTTCTTCTTGAAGCACTTTGGGGCATGGTTGAGGT-----GACAAAG 297
Oy      26  ValLeuValTrpProCysAspMetSerHisTrpLeuAsnValLysValIleLeuGlnGlu 45
Db      298  CTGCTGGGGTCCCTCAGAGAGCGAAGCCACTGCTTAGATGAAAGATATTAAGTTAGGTT 357
Oy      46  IleIleValArgGlnIleGluValThrValLeuThrHisSerLysProSerLeuLeuAsp 65

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